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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/075,460

DATE: 03/01/2002
TIME: 11:45:56

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Output Set: N:\CRF3\03012002\J075460.raw

2.

3 <110> APPLICANT: MOCKEL, BETTINA
 4 BATHE, BRIGITTE
 5 HANS, STEFAN
 6 KREUTZER, CAROLINE
 7 HERMANN, THOMAS
 8 PFEFFERLE, WALTER
 9 BINDER, MICHAEL
 11 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
 13 <130> FILE REFERENCE: 218472US0X
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/075,460
 C--> 15 <141> CURRENT FILING DATE: 2002-02-15
 15 <150> PRIOR APPLICATION NUMBER: DE 10107230.9
 16 <151> PRIOR FILING DATE: 2001-02-16
 18 <150> PRIOR APPLICATION NUMBER: DE 10162386.0
 19 <151> PRIOR FILING DATE: 2001-12-19
 21 <160> NUMBER OF SEQ ID NOS: 14
 23 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1775
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Corynebacterium glutamicum
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (500)..(880)
 33 <223> OTHER INFORMATION:
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 41 tcggtaagg tcagtgccgaa gttctttgc tggtcgttt ctttggaa cagtcatggg 180
 43 aaccattcta acaaggatt tggtggatt tgccgttagc tgataatgtg aacggctgag 240
 45 tcccactttt gtagttggaa attgacggca cctcgactc aagcgccgtt tcgccttgg 300
 47 ttttccggaa cgcgtggcg catgtttgaa tttgatgagg ttgtccgtt catgtttgg 360
 49 cggcccccaa aaagagcccc ctttttgcg tgtctggaca ctttttcaaa tccttcgcca 420
 51 tcgacaagct cagccttcgt gttcgcccc cggcgctcac gtcagcagtt aaagaacaac 480
 53 tccgaaataa ggtatggttc atg cca act att cag cag ctg gtc cgt aag ggc 532
 54 Met Pro Thr Ile Gln Gln Leu Val Arg Lys Gly
 55 1 5 10
 57 cgc cac gat aag tcc gcc aag gtg gct acc gcg gca ctg aag ggt tcc 580
 58 Arg His Asp Lys Ser Ala Lys Val Ala Thr Ala Ala Leu Lys Gly Ser
 59 15 20 25
 61 cct cag cgt cgt ggc gta tgc acc cgt gtg tac acc acc acc cct aag 628
 62 Pro Gln Arg Arg Gly Val Cys Thr Arg Val Tyr Thr Thr Pro Lys
 63 30 35 40

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175	tcggtaagg tcagtggcga gcttctttgc tggtcgttt cttgaggaa cagtcatggg	180		
177	aaccattcta acaaggatt tggtgtttc tgcggctagc tgataatgtg aacggctgag	240		
179	tcccactttt gtagttggga attgacggca ctcgcactc aagcgcggta tcgccttgg	300		
181	ttttccggga cgcggtggcg catgtttgca tttgatgagg ttgtccgtga catgtttgg	360		
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185	tcgacaagct cagccctcgt gttcgcccc cggcgtcac gtcagcagtt aaagaacaac	480		
187	tccgaaataa ggtgggttc atg cca act att cag cag ctg gtc cgt aag ggc	532		
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191	cgc cac gat aag tcc gcc aag gtg gct acc gcg gca ctg aag ggt tcc	580		
192	Arg His Asp Lys Ser Ala Lys Val Ala Thr Ala Leu Lys Gly Ser			
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195	cct cag cgt cgt ggc gta tgc acc cgt gtg tac acc acc acc cct agg	628		
196	Pro Gln Arg Arg Gly Val Cys Thr Arg Val Tyr Thr Thr Pro Arg			
197	30 35 40			
199	aag cct aac tct gct ctt cgt aag gtc gct cgt gtg cgc ctt acc tcc	676		
200	Lys Pro Asn Ser Ala Leu Arg Lys Val Ala Arg Val Arg Leu Thr Ser			
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203	ggc atc gag gtt tcc gct tac atc cct ggt gag ggc cac aac ctg cag	724		
204	Gly Ile Glu Val Ser Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln			
205	60 65 70 75			
207	gag cac tcc atg gtg ctc gtt cgc ggt cgt gtt aag gac ctc cca	772		
208	Glu His Ser Met Val Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro			
209	80 85 90			
211	ggt gtc cgt tac aag atc gtc cgt ggc gca ctg gat acc cag ggt gtt	820		
212	Gly Val Arg Tyr Lys Ile Val Arg Gly Ala Leu Asp Thr Gln Gly Val			
213	95 100 105			
215	aag gac cgc aag cag gct cgt tcc ccg cta cgg cgc gaa gag ggg ata	868		
216	Lys Asp Arg Lys Gln Ala Arg Ser Pro Leu Arg Arg Glu Glu Gly Ile			
217	110 115 120			
219	att aaa aat gcg taaatcagca gtccttaagc gtccagtagt tcaggaccct	920		
220	Ile Lys Asn Ala			
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227	gatccagtag	gaaccctcg	gaaggctctc	ggcaacgtgc	gtccagacct	cgaagttcgt	1100											
229	tcccgccgt	ttggtggcgc	tacctaccag	gtgcaggatgg	atgttcgccc	agagcgcgca	1160											
231	aacaccctcg	cactgcgtt	gttggtaacc	ttcacccgtc	agcgtcgtga	gaacaccatg	1220											
233	atcgagcgtc	ttgcaaacga	acttctggat	gcagccaacg	gccttggcgc	ttccgtgaag	1280											
235	cgtcgcgaag	acacccacaa	gatggcagag	gccaacccgc	cttcgctca	ctaccgctgg	1340											
237	tagtactgcc	aagacatgaa	agcccaatca	ccttaagat	caacgcctgc	cggccccc	1400											
239	cacatttcaa	taagctggca	gcctgcgtt	cttcaaggcg	actgggc	ttttactgt	1460											
241	aatgcagttc	accgcgttaa	gatagctaaa	tagaaacact	gttgcggcag	tgtttaacta	1520											
243	aaaaatccat	gtcacttgcc	tcgagcgtgc	tgcttgaatc	gcaagttag	ggcaaaatgt	1580											
245	aacaagagaa	ttatccgtag	gtgacaaact	ttttaatact	tgggtatctg	tcatggatac	1640											
247	cccggtataa	aataagtcaa	ttaccgttaac	caacaagttg	gggttaccact	gtggcacaag	1700											
249	aagtgtttaa	ggatctaaac	aaggccgca	acatccgcac	catggcgcac	atcgatgctg	1760											
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265	Ala	Lys	Val	Ala	Thr	Ala	Ala	Leu	Lys	Gly	Ser	Pro	Gln	Arg	Arg	Gly		
266					20				25					30				
269	Val	Cys	Thr	Arg	Val	Tyr	Thr	Thr	Pro	Arg	Lys	Pro	Asn	Ser	Ala			
270					35				40					45				
273	Leu	Arg	Lys	Val	Ala	Arg	Val	Arg	Leu	Thr	Ser	Gly	Ile	Glu	Val	Ser		
274					50				55					60				
277	Ala	Tyr	Ile	Pro	Gly	Glu	Gly	His	Asn	Leu	Gln	Glu	His	Ser	Met	Val		
278		65			70					75					80			
281	Leu	Val	Arg	Gly	Gly	Arg	Val	Lys	Asp	Leu	Pro	Gly	Val	Arg	Tyr	Lys		
282					85				90					95				
285	Ile	Val	Arg	Gly	Ala	Leu	Asp	Thr	Gln	Gly	Val	Lys	Asp	Arg	Lys	Gln		
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309	tcgacgcctc	cctcgacgt	gtcgtgtct	ctaagctgtt	tgcacacggcc	gaaaggcatcc									180			
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321	ctctgagtcg	ttgcgttga	attcgtgact	cttttcgtt	cctgtacgc	caagaccttgc	540			
323	atcaagggtgg	tttaaaaaaa	ccgatttgcac	aaggtcattc	agtgcatact	ggatcggttc	600			
325	agggggatcg	gttccctcag	cagaccaatt	gctaaaaat	accagcgttgc	ttgatctgca	660			
327	cttaatggcc	ttgaccagcc	agggtcaatt	accgcgtga	g	gtg ctg gaa gga ccc	716			
328					Val	Leu	Glu	Gly	Pro	
329					1		5			
331	atc ttg	gca gtc	tcc cgc	cag acc	aag tca	gtc gtc	gat att	ccc ggt		764
332	Ile Leu	Ala Val	Ser Arg	Gln Thr	Lys Ser	Val Val	Asp Ile	Pro Gly		
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335	gca ccg	cag cgt	tat tct	ttc gcg	aag gtg	tcc gca	ccc att	gag gtg		812
336	Ala Pro	Gln Arg	Tyr Ser	Phe Ala	Lys Val	Ser Ala	Pro Ile	Glu Val		
337				25		30		35		
339	ccc ggg	cta cta	gat ctt	caa ctg	gat tct	tac tcc	tgg ctg	att ggt		860
340	Pro Gly	Leu Leu	Asp Leu	Gln Leu	Asp Ser	Tyr Ser	Trp Leu	Ile Gly		
341				40		45		50		
343	acg cct	gag tgg	cgt gct	cgt cag	aag gaa	gaa ttc	ggc gag	gga gcc		908
344	Thr Pro	Glu Trp	Arg Ala	Arg Gln	Lys Glu	Glu Phe	Gly Glu	Gly Ala		
345				55		60		65		
347	cgc gta	acc agc	ggc ctt	gag aac	att ctc	gag gag	ctc tcc	cca atc		956
348	Arg Val	Thr Ser	Gly Leu	Glu Asn	Ile Leu	Glu Leu	Glu Leu	Ser Pro Ile		
349	70			75		80		85		
351	cag gat	tac tct	gga aac	atg tcc	ctg agc	ctt tcg	gag cca	cgc ttc		1004
352	Gln Asp	Tyr Ser	Gly Asn	Met Ser	Leu Ser	Leu Ser	Glu Pro	Arg Phe		
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355	gaa gac	gtc aag	aac acc	att gac	gag gcg	aaa gaa	aag gac	atc aac		1052
356	Glu Asp	Val Lys	Asn Thr	Ile Asp	Glu Ala	Lys Glu	Lys Asp	Ile Asn		
357				105		110		115		
359	tac gcg	gct cca	ctg tat	gtg acc	gct gag	ttc gtc	aac aac	acc acc		1100
360	Tyr Ala	Ala Pro	Leu Tyr	Val Thr	Ala Glu	Phe Val	Asn Asn	Thr Thr		
361				120		125		130		
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372	Ser Gln	Leu Val	Arg Ser	Pro Gly	Val Tyr	Phe Asp	Gln Thr	Ile Asp		
373				170		175		180		
375	aag tca	act gag	cgt cca	ctg cac	gcc gtg	aag gtt	att cct	tcc cgt		1292
376	Lys Ser	Thr Glu	Arg Pro	Leu His	Ala Val	Lys Val	Ile Pro	Ser Arg		
377				185		190		195		
379	ggt gct	tgg ctt	gag ttt	gac gtc	gat aag	cgc gat	tcg gtt	ggt gtt		1340
380	Gly Ala	Trp Leu	Glu Phe	Asp Val	Asp Lys	Arg Asp	Ser Val	Gly Val		
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VERIFICATION SUMMARY
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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date